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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                               SPTREMBL_15:*
                                                                                                                                                                                                                                                                                                                                                                                                                                       374700 seqs, 117207915 residues
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248
1 NQEDPQTECQQCQRRCRQQE......RQQQYCQRRCKEICEEEEEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 1, 2001, 16:08:59; Search time 299.73 Seconds (without alignments) 16.815 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
sp_fungi:*
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sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | U | 4 | ω | 2 | ۳ | Result No. |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|-----------------------|
| 73.5 | 73.5 | 73.5 | 74 | 74 | 74 | 74 | 75 | 77.5 | 79 | 80.5 | 80.5 | 80.5 | 96 | 117 | 119 | 241 | 242 | 248 | Score |
| 29.6 | 29.6 | 29.6 | 29.8 | 29.8 | 29.8 | 29.8 | 30.2 | 31.2 | 31.9 | 32.5 | 32.5 | 32.5 | 38.7 | 47.2 | 48.0 | 97.2 | 97.6 | 100.0 | Query Match Length |
| 419 | 335 | 335 | 445 | 438 | 388 | 388 | 339 | 242 | 572 | 810 | 600 | 425 | 411 | 525 | 593 | 625 | 666 | 666 | |
| U | ÇΊ | Çī | Ŋ | Ų | Çī | υī | Çī | Ŋ | υ | 10 | S | G | ഗ | 10 | 10 | 10 | 10 | 10 | DB |
| Q9NA38 | Q9NF69 | Q9NF70 | 016511 | 016502 | 016501 | 016500 | Q9N4R1 | Q19919 | Q19594 | Q9ZWI3 | Q17401 | Q17400 | P91419 | Q43358 | Q9SEW4 | Q9SPL3 | Q9SPL4 | Q9SPL5 | ID |
| Q9na38 caenorhabdi | Q9nf69 caenorhabdi | Q9nf70 caenorhabdi | 016511 caenorhabdi | 016502 caenorhabdi | 016501 caenorhabdi | 016500 caenorhabdi | Q9n4r1 caenorhabdi | Q19919 caenorhabdi | Q19594 caenorhabdi | Q9zwi3 cucurbita m | Q17401 caenorhabdi | Q17400 caenorhabdi | P91419 caenorhabdi | _ | Q9sew4 juglans reg | Q9spl3 macadamia i | Q9spl4 macadamia i | Q9spl5 macadamia i | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|-------------------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|
| 61 | 62 | 62 | 62 | 62 | 62.5 | 63 | 63 | 63 | 65 | 65 | 65 | 66.5 | 66.5 | 66.5 | 66.5 | 68 | 68.5 | 68.5 | 70 | 70.5 | 71.5 | 72.5 | 72.5 | 73 | 73.5 |
| 24.6 | | | | | | | | 25.4 | | | | | | | | | | | | | | | | 29.4 | 29.6 |
| 400 | 1080 | 715 | 648 | 425 | 342 | 910 | 910 | 243 | 1306 | 539 | 111 | 637 | 356 | 314 | 273 | 594 | 654 | 393 | 1513 | 378 | 335 | 709 | 330 | 388 | 420 |
| σ | G | 4 | G | ഗ | 4 | 11 | 11 | ن | ഗ | 4 | | _ | | | | | | _ | | | | | | S | G |
| Q95337 | Q9N2M8 | Q9UEX4 | Q9TXB8 | 015755 | Q9UK28 | 088704 | 054899 | Q9NL90 | 077273 | Q9NUA2 | Q19054 | Q03678 | Q17316 | Q23390 | 045362 | 077337 | Q17982 | Q92TP0 | 017970 | Q27383 | Q9N6L3 | Q9N4R2 | 018118 | 044606 | Q9NA61 |
| | _ | | _ | | _ | 088704 mus musculu | 054899 mus musculu | Q9n190 entamoeba d | 077273 drosophila | | Q19054 caenorhabdi | Q03678 hordeum vul | Q17316 ceratitis c | | 045362 caenorhabdi | | Q17982 caenorhabdi | Q9ztp0 oryza sativ | 017970 caenorhabdi | | | Q9n4r2 caenorhabdi | 018118 caenorhabdi | 044606 caenorhabdi | Q9na61 caenorhabdi |

ALIGNMENTS

| RESULT Q9SPL4 ID Q AC Q DT 0 | Qy Db | K # 10 | DR SQ | DR | DR DR | R. | R 2 | RA | R i | RP X | XOX | 8 | 8 | 0 2 | DE | DT | DT | DT | AC | ID O | RESULT |
|---|--|--|---|----|-----------------------------|-----------------------|---|--------|--------------------|--------------------|------------------|--------------------------------------|---|--|--------------------|-----------|-----------------|------------------|----|----------------------------------|--------|
| LIT 2 Q9SDL4 PRELIMINARY; PRT; 666 AA. Q9SSL4; Q1-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) | MATCHES 43; CONSERVATIVE 0; MISMATCHES 0; Indels 0; Gaps 0; 1 NQEDPQTECQQCQRCRQQESGPRQQQYCQRRCKEICEEEEEV 43 | atch 100.0%; Score 248; DB 10; Length 666; cal Similarity 100.0%; Pred. No. 1.2e-22; | PFAM; PF00546; Seedstore_7s; 1. SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64; | | EMBL; AF161883; AAD54244.1; | Plant J. 0:0-0(1999). | alobulin protein in Macadamia integrifolia kernels.": | h h | TISSUE=NUT KERNEL; | SEQUENCE FROM N.A. | C2I_TaxID=60698; | dicotyledons; Proteaceae; Macadamia. | Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; | Macadamia integrifolia (Macadamia put) | VICILIN PRECURSOR. | Lrel. 15, | (TrEMBLrel, 13, | 2000 (TrEMBLrel. | | O9SPL5 PRELIMINARY; PRT; 666 AA. | וביי 1 |
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(TrEMBLrel.

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Last annotation update)

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RESULT
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Q9SEW4;
Q9SEW4;
01-MAY-2000
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01-MAY-2000 (
01-MAY-2000 (
01-OCT-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marcus J.P., Goulter K.C., Green J.L., Manners J
"A family of antimicrobial peptides is produced
globulin protein in Macadamia integrifolia.";
plant J. 0.-0(1999).
EMBL; AF161885; AAD54246.1; -.
HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
"A family of antimicrobial peptides is produced by p
globulin protein in Macadamia integrifolia.";
plant J. 0:0-0(199).
EMBL; AF161884; AAD54245.1; -.
HSSP; P02853; 2PHL.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
NCBI_TaxID=60698;
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO01113; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=NUT KERNEL;
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                                                                                                                                                                                       NQDDPQTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEY
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PF00546; Seedstore_7s;
NCE 666 AA; 78243 MW
                                                                                                                                                                                                                                                                                   l Similarity
42; Conserv
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41; Conservative
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
(TrEMBLrel.
                                                                      PRELIMINARY;
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97.7%;
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Last seq
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Pred. No. 6.5e-22;
2; Mismatches 0;
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Q43358;
Q1-NOV-1996
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                 McHenry L., Fritz P.J.;

"Comparison of the structure and nucleotide sequences of vicilin of cocoa and cotton raise questions about vicilin evolution.";

Plant Mol. Biol. 18:1173-1176(1992).

EMBL; X62625; CAA44493.1; -..

EMBL; X62625; CAA44494.1; -..

EMBL; X62625; CAA44494.1; -..
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Eukaryota; Viridiplantae; Embr
Magnoliophyta; eudicotyledons;
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STRAIN-CV. SUNLAND; TISSUE-SOMATIC EMBRYO LINE;
Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
"Identification and cloning of a cDNA encoding a vicilin-like protei
Jug r 2, from English walnut kernel (Juglans regia): a major food
allergen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
Juglans regia (English walnut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta
Magnoliophyta; eudicotyledons; core eudicots; Rosid
Fagales; Juglandaceae; Juglans.
NCBI_TaxID-51240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VICILIN PRECURSOR.
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                            PRODOM; PD081059; -;
                                                                                                                                                                                                                                                                        PFAM; PF00546;
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                                                                                                                                                                                                                                                                                                                   MENDEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malvales; Malvaceae;
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2 QEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEE
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                                           ch 47.2%; Similarity 50.0%; 20; Conservative 1
                                                                                                                                                                                                                                                                                                                   30919;
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                                             10;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 119; DB Pred. No. 5.3e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases.
                                                                Score 117;
Pred. No. 8
                                                                                                                                                                                   VICILIN
                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                            19114CD5C248905D CRC64;
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                                             Mismatches
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5.
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                                             10;
    41
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01-JAN-1999 (
01-JAN-1999 (
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
HYPOTHETICAL 45.9 KDA PROTEIN AC3.3 IN CHROMOSOME V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C
                                                                                                Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                          Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R;
Water
                                                 SEQUENCE FROM N.
                                                                                                                                                                      Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                      Q17400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BRISTOL N2;
Bradshaw H., Wohldmann F
Submitted (JAN-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1998 (TrEMBLrel.
CODED FOR BY C. ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                    Nematoda;
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39.5%;
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03, 1
08, I
                                                                                                                          cda; Chromadorea;
Caenorhabditis.
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Pred. No. 0.00
L1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence up Last annotation A YK115A6.5.
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                                                                                                                                              Rhabditida; Rhabditoidea
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RESULT
Q9ZWI3
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AC Q9
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Best Local S
Matches 17
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Best Local
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Q17401;
01-JAN-1999
01-JAN-1999
01-JUN-2000
                                                                                                                                                              TRANSMEM
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO FAMILY UPF.
EMBL; 771177; CAA94867.1; -.
WORMPEP; AC3.3; CE05133.
Hypothetical protein; Signal.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 425 HYPOTHETICAL PROTEIN AC3.3.
                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                    Mcmurray A.
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                                                   182
                                                                                                                                                                                                                                  INTERPRO;
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                                                   182
                                                                   39
                                                                                                                    ch 32.5%; l Similarity 27.9%; 17; Conservative
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17; Conserv
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22
425 A
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(TrEMBLrel. 09, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
L 67.7 KDA PROTEIN AC3.4 IN CHROMOSOME V.
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                               AA;
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510
287
67740 N
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45922 MW;
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                                                                                                                                                               WW.
                                                                                                                   Score 80.5; Depred. No. 0.02
9; Mismatches
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Pred. No. 0.01
9; Mismatches
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                                                                                                                                                           GLN-RICH.
; 504A5CE1BA72091B CRC64;
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HYPOTHETICAL PROTEIN AC3.3.
; 951352A2AFF7E96C CRC64;
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                                                                                                                                                                                                                                                                                                                                    Rhabditoidea
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                                                                                                                   Gaps
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                                                                                  181
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Q9ZWI3;

PRELIMINARY;

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2

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RESULT 11
Q19919
ID Q19919
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Q19594
AC Q1
DT Q
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Best I
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Best Local S
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Q19594;
Q1-JUN-1998
Q1-JUN-1998
Q1-CCT-2000
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01-MAY-1999
01-OCT-2000
PV100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrembLrel. 06, Created)
01-JUN-1998 (TrembLrel. 06, Last sequence update)
01-OCT-2000 (TrembLrel. 15, Last annotation update)
HYPOTHETICAL 62.4 KDA PROTEIN F19G12.7 IN CHROMOSOME X PRECURSOR.
F19G12.7.
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
Nhan M., Le T.T.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ
-!- SIMILARTTY: BELONGS TO FAMILY UPF.
EMBL; U51997; AAC48159.1; -.
WORMPEP; F19G12.7; CE07090.
                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Signal.
SIGNAL 1 21
CHAIN 22 572
SEQUENCE 572 AA; 62384 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
[1]
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00546; Seedstore_7s; PRODOM; PD081059; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB019195; BAA34056.1; HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada K., Shimada T., Kondo M., Nishimura M., Hara-Nis
"Multiple functional proteins are produced by Cleaving
of a single precursor by vacuolar processing enzyme.";
J. Biol. Chem. 274:2563-2570(1999).
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MEDLINE-99107919; PubMed-9891029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
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                                                                                                                                                             ECQQCQRRCRQ---
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Pred. No. 0.03
9; Mismatches
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89
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HYPOTHETICAL PROTEIN F19G12.7.
BDA5B2FDB850AAB9 CRC64;
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3; Mismatches
                                                                                                                                                                                                                                                   Score
    PRT;
                                                                                                                                                           -QESGPRQQQYCQRRCKE---ICEEE 40
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09N4R1;
01-OCT-2000
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01-JUN-1998
01-JUN-1998
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01-JUN-1998 (TremBLrel. 06, Last sequence update)
01-JUN-1998 (TremBLrel. 06, Last annotation update)
HYPOTHETICAL 26.2 KDA PROTEIN F31A3.1 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Cae
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN Y5H2A.C.
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WORMPEP; F31A3.1; CE07158.
Hypothetical protein; Transmembrane.
TRANSMEM 3 23 POTENTI
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NCBI_TaxID=6239;
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MEDLINE=99069613; PubMed=9851916;
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Science 282:2012-2018(1998).
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   167
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QQASAPQCQQCQNTCQQFAPVCQQQCAPQCTISSAPQCQQCQTTCQQFAPVCQQQ 221
                                                                 QEDPQTECQQCQRRCR----
                                                                                                                                                                                                                                                                                                       AC006809; AAI
NCE 339 AA;
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l6; Conservative
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                                                                                                                                                                                                                                                                                                   2000) to the EMBL/GenBank/DDBJ
AAF59626.1; -.
AA; 36218 MW; 40233423237C43:
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Caenorhabditis.
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                                                                 -QQESGPR----
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0.075;
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O16500;
O1-JAN-1998 (TrEW
O1-JAN-1998 (TrEW
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CO3A7.4 PROTEIN.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Bonfield J., Burton J., Connell M., Copsey T., Cooper J.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Mortinore B., O'Callaghan M.,
Lightning J., Illyd C., Mcmurray A., Mortinore B., O'Callaghan M.,
Lightning J., Illyd C., Riken L., Ropera A., Saunders D., Shownkeen I
Barsons J., Percy C., Riken L., Ropera A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson S., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Staden B., Staden R., 
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
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    Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Cou
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnst
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                  STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                 Rhabditidae;
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                                                                                                                                          SEQUENCE FROM N.A.
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AF016451; AAB66001.1; -
NCE 388 AA; 42139 MW; 2E20655B0B9AE492 CRC64;
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Caenorhabditis.
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                                  Johnston L.,
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"2.2 Mb of contiguous
elegans.";
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MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF016451; AAB65995 1; SEQUENCE 438 AA; 47502 MW; 835C4F68ECF510B1 CRC64;
                                                                                                                Waterston R.;
                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                       Greco T.,
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